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Abstract

As COVID-19 has spread across the globe, several observers noticed that countries still administering an old vaccine against tuberculosis—the BCG vaccine—have had fewer COVID-19 cases and deaths per capita in the early stages of the outbreak. This paper uses a geographic regression discontinuity analysis to study whether and how COVID-19 prevalence changes discontinuously at the old border between West Germany and East Germany. The border used to separate two countries with very different vaccination policies during the Cold War era. We provide formal evidence that there is indeed a sizable discontinuity in COVID-19 cases at the border. However, we also find that the difference in novel coronavirus prevalence is uniform across age groups and show that this discontinuity disappears when commuter flows and demographics are accounted for. These findings are not in line with the BCG hypothesis. We then offer an alternative explanation for the East-West divide. We simulate a canonical SIR model of the epidemic in each German county, allowing infections to spread along commuting patterns. We find that in the simulated data, the number of cases also discontinuously declines as one crosses from west to east over the former border.

Key words: COVID-19, BCG vaccine, SIR model with commuting flows

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1 Introduction

As COVID-19 has spread across the globe, there is an intense search for treatments and vaccines, with numerous trials running in multiple countries. In light of this, there is now a lively controversy over whether the Bacillus Calmette-Guérin (BCG) vaccine against tuberculosis may somehow protect individuals against COVID-19 or limit its severity. Multiple studies (see, e.g., Miller et al., 2020, Berg et al., 2020) pointed out that countries with mandatory BCG vaccination tend to have substantially fewer coronavirus cases and deaths per capita than countries without mandatory vaccination, and that the intensity of the epidemic is lower for countries that began vaccinating earlier.[1] At least eight clinical trials are taking place across the globe[2] in which some medical workers or volunteers receive the BCG vaccine to test its effectiveness against COVID-19. These trials are likely to take at least a year and the virus is still spreading globally at a rapid pace. As of now, the WHO cautions that there is no evidence that the vaccine protects against the novel coronavirus.[3]

In this paper we propose a different way to test the hypothesis that BCG protects a large share of vaccinated populations against coronavirus: a regression discontinuity analysis of coronavirus cases at the former border between East Germany and West Germany. This border separated capitalist West Germany from communist East Germany from 1949 to 1990 until the two countries were reunified as the current Federal Republic of Germany. In line with many other Western European countries, West Germany discontinued a policy of de facto universal BCG vaccination (which began in the 1950s) for the general population in 1975, while, equally in line with other former Soviet Bloc countries, East Germany strictly enforced a policy of mandatory BCG vaccination at birth from 1953 until 1990. Although it is known that other characteristics change discontinuously at the old East German border (even before it existed, see Becker et al., 2020, Fuchs-Schündeln and Hassan, 2015, Alesina and Fuchs-Schündeln, 2007), these differences are considerably smaller than if different countries or regions are compared. Moreover, areas of Germany on both sides of the discontinuity have been subject to the same state response to the COVID-19 pandemic. Other discontinuities

[1] This started a lively debate in the community on the fallacies of cross-country regressions. As our approach differs from these studies, we only note that other studies which are not based on cross-country data find no such effects, for example when looking at passengers on the Diamond Princess or when controlling for countries' intensity of testing for COVID-19 (Asahara, 2020).

[2] For example, the BRACE trial in Australia (NCT04327206), the BCG-CORONA trial in the Netherlands (NCT04328441), and more recent trials in Brazil (NCT04369794), Columbia (NCT04362124), Denmark (NCT04373291), Egypt (NCT04350931) and the United States (NCT04348370). ClinicalTrials.gov registry codes are provided in parentheses.

[3] This warning was based on a review of the available evidence from three cross-country studies. The scientific briefing is published here (www.who.int/publications-detail/bacille-calmette-gu%C3%A9rin-(bcg)-vaccination-and-covid-19) and explained further in Curtis et al. (2020).

are also less of a concern since we can exploit variation both in space and across age groups to improve identification.

We find a strong discontinuity in cumulative COVID-19 cases across the old East German border, with cases per million roughly halving at the border as of April 26 2020. This discontinuity is robust to controlling for other variables that change discontinuously at the border, such as population density, disposable income, average age and the fraction of the population over 65, as well as age-adjusted death rates from all causes and from infectious diseases.[4] Importantly, while these control variables are discontinuous at the border, the discontinuities typically go the "wrong way" in terms of their correlations with characteristics that usually indicate more vulnerable populations. Counties on the eastern side of the border are poorer, older and have higher death rates, although they have lower population density, than counties just to the west of the border. We document that the initial geography of the outbreak in wealthier and well-connected places implies that these correlations are reversed from what intuition would suggest. For example, the outbreak is currently stronger in richer, younger and generally healthier places of Germany.

Evidence from discontinuities in COVID-19 confirmed cases by age group suggests that this discontinuity does not come from people on the eastern side of the border being protected by the BCG vaccine. The timing of the adoption and the cessation of mandatory vaccination in East and West Germany implies that the only age groups for which discontinuities should be observed should be individuals between ages 30 and 45, as well as people between ages 59 and 69. For other age groups, there should be no direct effect of the BCG vaccine since they were either unvaccinated or vaccinated on both sides of the border. However, there is a discontinuous decrease in COVID-19 confirmed cases of approximately the same size as one crosses the border into the east for every age group for which we have data, starting with individuals who are 15 years old (people younger than 15 rarely manifest strong enough COVID-19 symptoms to get tested).[5]

We provide further evidence on what could be giving rise to the discontinuity in coronavirus cases at the old border to East Germany by considering the matrix of commuter

[4]Prominent newspapers in Germany have noticed that there is much lower COVID-19 prevalence in the former East than in the West but offer only suggestive explanations (e.g., *Die Zeit*, a German weekly, www.zeit.de/2020/13/coronavirus-ausbreitung-osten-westen-faktoren, or *Der Tagesspiegel*, a Berlin-based German daily, www.tagesspiegel.de/politik/mehr-flaeche-mehr-alte-warum-der-osten-weniger-unter-corona-leidet/25796940.html). Moreover, low COVID-19 mortality in Germany as a whole has been the subject of media interest.

[5]One could expect that vaccinated individuals in a population offer some degree of protection to the unvaccinated. In fact, medical research (Curtis et al., 2020) suggests that there may be a countervailing effect as BCG-vaccinated places may have more asymptomatic individuals with a greater propensity to spread the virus. Even if the overall spillover did offer protection to unvaccinated individuals, the resulting discontinuity for such individuals should be smaller than for the population affected directly by the vaccine.

flows across German counties. Apart from strong connections between major cities in the West and Berlin, these flows still generally proceed within the former West or within the former East rather than between both sides. Since the epidemic started in the West, these flows imply that it was more likely that it would be transmitted more rapidly and widely there than in the East. We simulate a SIR model with mobility flows between counties to asses how mobility patterns shaped the geography of the pre-lockdown outbreak. In line with our empirical evidence, we find that the model also generates a discontinuity at the border, with more cases per capita on the western side relative to the eastern side, without any reference to the BCG hypothesis.

An important caveat is that our study looks only at whether or not there is a long-run effect of the BCG vaccine (roughly decades after it was administered). The BCG hypothesis essentially comes in two variants. The broad version suggested by cross-country correlations hypothesizes that people who have received this vaccine in the past (perhaps with refreshers) develop no or comparatively milder symptoms of COVID-19 than those who have not, enough for this to show up in the incidence of novel coronavirus cases around the world. If this were true, the BCG vaccine would provide a respite to the developing world as the virus spreads globally, which is why prominent news outlets have reported this correlation.[6] This is the question we address in this paper. However, the BCG vaccine's positive effect on other viral infections, such as yellow fever (Arts et al., 2018), is a trained response of the immune system typically occurring within one to twelve months after it has been administered. The evidence of such trained responses is mixed (for a review see Kandasamy et al., 2016) although recently a consensus seems to have emerged that the protective effects on other diseases occur via epigenetic reprogramming (Kleinnijenhuis et al., 2015, Covián et al., 2019). The narrow version of the hypothesis suggests that the vaccine might have a short-run effect which could offer some protection to health workers and other risk groups. Our research design cannot test this aspect as the vaccine has been discontinued in both parts of Germany for 30 years. Only the results from randomized trials can answer that question.

The remainder of the paper is organized as follows. Section 2 describes the county-level data on cases, covariates, and commuter flows. Section 3 discuses the temporal differences in BCG policies in Germany from partition to reunification and describes our empirical strategy. Section 4 presents the results for discontinuities in overall cases, the most relevant covariates, cases by age-groups, and the placebo test with cases simulated from a county-level SIR model with mobility. Section 5 concludes.

[6] See, for example, *The New York Times* (www.nytimes.com/2020/04/03/health/coronavirus-bcg-vaccine.html) or *Bloomberg News* (www.bloomberg.com/news/articles/2020-04-02/fewer-coronavirus-deaths-seen-in-countries-that-mandate-tb-vaccine).

2 Data

COVID-19 spread in Germany: We obtain counts of cumulative cases of and deaths from COVID-19 by German county (*Kreis*) and by age group for every date since February 29 2020 from the Robert Koch Institute's Coronavirus Dashboard.[7] Germany has one of the most comprehensive testing regimes among the heavily affected countries.[8] Nevertheless, given the difficulties in recording asymptomatic cases of COVID-19 that may still be contagious, it is very likely that the case counts we employ in this paper are a lower bound for novel coronavirus infections in Germany.[9] Streeck et al. (2020) study a large sample of the city of Heinsberg—a community with an early a super-spreading event—and estimate that the true case count is about five times larger than officially registered cases. We proceed on the necessary assumption that the cumulative reported case count is a valid measure of COVID-19 intensity in a given subpopulation, and that undercounting errors are uniform across age groups and locations.

We start our analysis with a map of COVID-19 cases in Germany by county as of April 26 (see Figure 1). The former border between East and West Germany is outlined in red. The darker the shading of a county, the more novel coronavirus cases per million inhabitants it has. Several counties with high concentrations stand out (such as Heinsberg, bordering the Netherlands, and much of Bavaria, both places where the epidemic was first recorded). It is also clear that there is a greater density of COVID-19 cases around major cities (Berlin, Hamburg or Stuttgart), similar to the United States. However, we immediately see that counties just to the west of the former border are a much darker shade of blue than counties just to its east.

County-level covariates: We collect four groups of county-level characteristics: income and demographics, historical mortality, and commuting flows. Baseline characteristics of each county (shapes, names and areas) are from the Federal Agency for Cartography and Geodesy (*Bundesamt für Kartographie und Geodäsi*).

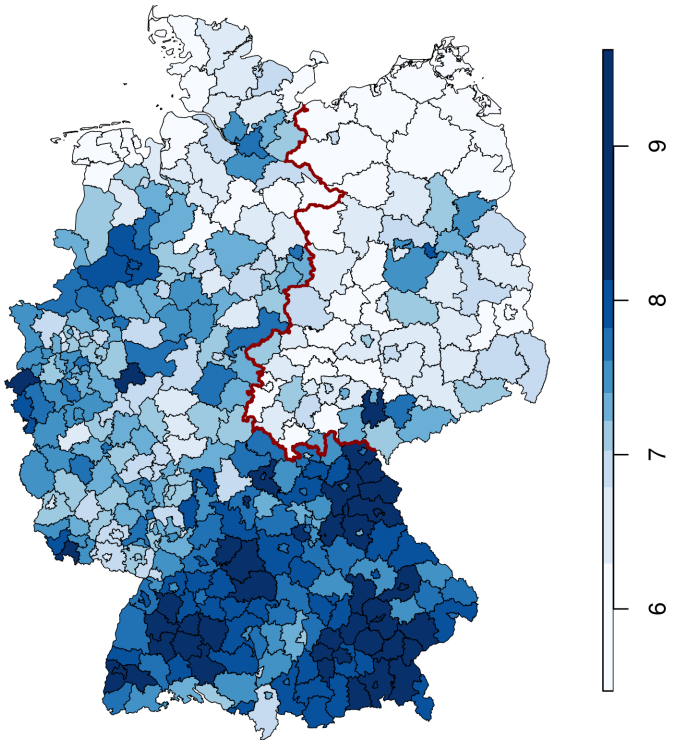
Measures of disposable income in 2017, the age distribution in 2018 (aggregated to different age groups or shares), and population density in 2018 are taken from official

[7] The data are publicly available at `corona.rki.de`.

[8] By April 21 2020, Germany had conducted 2,072,669 tests or about 24,966 tests per million people (Robert Koch-Institut, 2020). This is almost double the testing rate in the United States, United Kingdom or South Korea, see `www.businessinsider.com/coronavirus-testing-per-capita-us-italy-south-korea-2020-4`.

[9] These considerations may make it reasonable to treat cumulative case counts as an indication of the severity rather than of the incidence of COVID-19, since very mild cases, which may account for the majority of COVID-19 infections, typically do not lead to testing.

Figure 1 – Covid-19 cases in Germany, April 26 2020, log(1 + cases/million)



Notes: Illustration of the spatial distribution of COVID-19 cases in Germany as of April 26, 2020. The map shows the log(1 + cases/million people) in each county using population data from 2018.

statistics published by the federal statistical office and the statistical offices of each state.[10]

We also collect data on overall mortality (in 2017), mortality from selected infectious diseases and mortality from respiratory diseases (both in 2016) from the same source. Germany does not publish age-adjusted mortality figures. Given that the age-profile of the population varies significantly across counties in Germany, we manually age-adjust all mortality figures using the corresponding age distribution of the entire country in 2017 or 2016, respectively.[11] This allows us to analyze regional mortality differences net of local demographics.

Last but not least, we use the latest available data on commuting flows published by the Federal Employment Agency (*Bundesagentur für Arbeit*). The agency regularly releases an origin-destination matrix of commuting flows across German counties. These flows capture about 33 million officially registered jobs (all jobs with social security contributions). Approximately 39%, or 13 million, of the jobs are in a different county than the primary

[10]The data are available at `www.regionalstatistik.de/genesis`.

[11]The age-adjustment re-weights local mortality with the age profile of the entire country. We follow the direct method used by the U.S. Centers for Disease Control (Klein and Schoenborn, 2001).

tax residence of the employee. We use the county-to-county data from December 2019 to capture connections between western and eastern counties just before the outbreak of the novel coronavirus. While this cannot account for all travel flows around the outbreak perfectly, we assume that such unobserved flows follow the dominant pattern of employees returning home.[12]

3 Empirical Strategy

Our study exploits a discontinues change in vaccination policies across the former border dividing East and West Germany from 1949 until 1990.

Germany had a non-vaccination policy until the end of World War II and did not join Red Cross-led vaccination campaigns in the early post-war years, even though tuberculosis was widespread among the war-ravaged population.[13] BCG policies then diverged quickly when the country was divided. In 1953, the German Democratic Republic (GDR) introduced mandatory vaccination for a variety of diseases, including the BCG vaccine against tuberculosis.[14] The policy lasted until the collapse of the GDR in 1990. The Federal Republic of Germany only required mandatory vaccination for smallpox from 1949 until the end of 1975. The BCG vaccine was highly recommended but administered on a voluntary basis. In practice, vaccination of newborns was near universal by the mid-1960s.[15] In 1974, the policy was changed to vaccinate only children in risk groups and, in 1975, the BCG vaccine was temporarily withdrawn from the market in the West. Neo-natal vaccination practically ceased for two years (Genz, 1977). Voluntary vaccination of risk groups continued thereafter until 1998 (Robert Koch-Institut, 1976, 1998) but few people were vaccinated in West Germany from 1975 onward or in reunified Germany after 1990. Currently, no BCG vaccine is licensed in Germany. We summarize these political changes in Table 1. We use precisely these differences in vaccination policies across the former East and West, as well as

[12] A suitable alternative would be an origin-destination matrix derived from mobile phone movements through the early months of 2020. However, Germany's strong privacy protection laws have the side-effect that such products are rarely produced by private companies.

[13] This decision was in part due to the "Lübeck vaccination disaster" in which 251 infants were vaccinated with a BCG vaccine contaminated with live tuberculosis bacteria. Almost all children fell ill with tuberculosis and 72 died, leading the Interior Ministry to reject BCG vaccination as unsafe in 1930 (Loddenkemper and Konietzko, 2018).

[14] Enforcement in the GDR was strict. "From 1954 on, school children who had not yet been vaccinated had to present a letter of exemption not only from their parents but also from a physician" (Harsch, 2012, p. 420). Vaccinations substantially outstripped newborns in the early 1950s, suggesting that young adults born before the GDR existed where also vaccinated ex post.

[15] Due to the decentralized nature of the West German health care system, the initial roll out of the vaccination policy varied strongly by state in the 1950s. However, by 1964, practically all newborns in West Germany were BCG vaccinated shortly after birth (Kreuser, 1967).

across cohorts, to identify the effect of historical BCG vaccination on the spread of COVID-19 cases.

Table 1 – Timeline of vaccination policies in both parts of Germany, 1949 until today

Year	West Germany (FRG)	East Germany (GDR)
1949		First BCG vaccinations
1951-52		Extended program with GDR manufactured BCG vaccine
1953	BCG vaccine is licensed	Mandatory vaccination (with refresher), target rate at least 95%
1955	Recommendation to vaccinate all newborn children	
Mid 1960s	Near universal vaccination of newborns	Near universal vaccination of newborns
1974	Recommendation to only vaccinate children in risk groups	
1975	BCG vaccination temporarily halted	
1983	Further restriction to only those children that have TB in the family	
1988	Vaccine recommended only for children that tested negative for tuberculin and are risk groups	
1990	Reunification, policies of FRG continue	Reunification, policies of FRG apply
1998	Vaccination no longer recommended	

Notes: Based on Klein (2013) and various sources cited in the text.

We employ two related techniques to exploit these policy discontinuities. For our baseline estimates, we specify a spatial regression discontinuity (RD) design of the form

$$y_c = \alpha + \beta \textsc{East}_c + \delta_1 d_c + \delta_2 \left(d_c \times \textsc{East}_c\right) + \lambda_{s(c)} + \varepsilon_c \quad \text{if} \quad |d_c < b| \tag{1}$$

where c indexes counties (*Kreise*), y_c is the outcome variable, $\textsc{East}_c$ indicates whether the county was part of East Germany before reunification, d_c is the distance of county c from the former East German border (it is negative if $\textsc{East}_c = 0$ and positive if $\textsc{East}_c = 1$), and $\lambda_{s(c)}$ is a fixed effect for the border segment associated with county c. Border segments are defined as pairs of bordering states (*Bundesländer*). Note that we drop Berlin throughout the analysis and focus on the border separating the two larger countries, as Berlin in its entirety cannot be cleanly assigned to either East or West. Following Gelman and Imbens (2019), our specification uses an interacted local linear RD polynomial at a variety of plausible bandwidths b, ranging from 50 km to 200 km. We select this range by computing optimal bandwidths for the specification without border segment fixed effects according to various criteria developed in the literature (Imbens and Kalyanaraman, 2011, Calonico et al., 2014).

They vary by outcome but generally fall somewhere in the range between 80–200 km.

Spatial RD designs identify the causal effect directly at the border if three crucial assumptions hold (see, e.g., Dell, 2010). First, all other factors besides our treatment variable (BCG vaccination) should vary smoothly from counties just to the east and just to the west of the border at the time it was drawn. The strength of the RD approach is that it non-parametrically controls for these confounders, even if they are unobserved. Second, there should be no compound treatment, so that counties belonging to the West or East of the former border vary only according to the BCG regime. Third, there should be no selective sorting at the border at the time of the treatment. The first and second assumption are likely to be violated in our setting. As Becker et al. (2020) document, the post-war border is already visible in many economic variables before World War II and East Germany differed from West Germany in many more ways than its BCG vaccination policy. Selective sorting is unlikely during the Cold War years and was probably not motivated by the different BCG regimes, but selective migration did occur prior to the closing of the border in 1961. Hence, the simple discontinuity design presented in eq. (1) has a number of flaws.

We address these concerns by additionally exploiting the temporal discontinuity across cohorts. The RKI data reports COVID-19 cases for several cohorts, including those that are currently 15–34 or 35–59 years old. Table 1 shows that most members of the first age group did not get the vaccine anywhere. In the second group, everyone was vaccinated in the East but only those above 45 years old could have received the vaccine in the West if they were not part of the small risk group. The effect of pre-World War II confounders does not vary specifically across these two age groups and any compound treatment mostly affects the older cohort. We can therefore identify whether BCG vaccinations have an effect on the COVID-19 cases by simply comparing the regression coefficients across these two groups. Following Deshpande (2016), we can formalize this comparison by estimating a regression discontinuity differences-in-differences (RD-DD) specification

$$\begin{aligned} y_{c,a} = \; & \alpha_a + \beta \textsc{East}_c + \gamma \textsc{East}_c \times \textsc{Old}_a + \delta_1 d_c + \delta_2 d_c \times \textsc{East}_c + \\ & \delta_3 d_c \times \textsc{Old}_a + \delta_4 d_c \times \textsc{East}_c \times \textsc{Old}_a + \lambda_{s(c),a} + \varepsilon_{c,a} \quad \text{if} \quad |d_c < b| \end{aligned} \tag{2}$$

where a indexes age groups (15–34 and 35–59), $\textsc{Old}_a$ is an indicator for the age group 35–59, and the intercept and the border segment fixed effects are allowed to vary by age group. The coefficient of interest, γ, delivers an estimate of the difference in discontinuities across cohorts. The identification assumptions for this specification are less stringent than for the original RD design because we now allow discontinuities in other controls as long as they are the same across age groups. In particular, any compound treatment effects are differenced

out if they are the same at ages 15–34 and 35–59, and selective sorting at the border is allowed insofar as both age groups are sorting in the same way.

If the BCG hypothesis is true, then we would expect to see a negative discontinuity in cases for the older cohorts but no discontinuity or a much smaller discrepancy in the younger cohort. Finding a sizable discontinuity in both cohorts, or no differences in the discontinuity across cohorts, would be direct evidence against the broad version of the BCG hypothesis and an indication that something else is driving these results. As our data does not contain any age group which was recently vaccinated, we cannot assess whether the BCG vaccine has a short-run effect on those that were vaccinated within the last year.

4 Results

Baseline regression discontinuity results: To formalize the intuition of Figure 1, we use a regression discontinuity design, in which we nonparametrically estimate coronavirus prevalence as a function of the distance to the border and compare the estimates just to the east and just to the west of the border. Our main dependent variable is the logarithm of unity plus the number of cumulative COVID-19 cases per million in a German county as of April 26, 2020. As the average German county (*Kreis*) has about 200,000 inhabitants and nearly every Kreis has at least one confirmed COVID-19 case, this function behaves very similarly to the logarithm of cumulative cases per million. Figure 2 presents nonparametric estimates of the mean of the dependent variable by distance to the border of the former GDR, with positive distances indicating locations in former East Germany and negative distances corresponding to locations in former West Germany. We use a bandwidth of 100 km, which corresponds well to the optimal bandwidth (following Imbens and Kalyanaraman, 2011). We observe that while the nonparametric estimates are continuous to the left and to the right of zero, they are very discontinuous at zero with a downward jump of approximately 0.7 log points as one moves from west to east. This implies that there are half as many cases per capita in a former East German county relative to a West German county just across the border. This halving of cases dominates the variation in coronavirus prevalence among counties in the East (where it is uniformly low) and is sizable relative to the average prevalence in the West. Faraway counties in Bavaria (close to the early outbreaks in Italy) or near the borders with France and the Benelux countries have the highest cases.

The first row of Table 2 further formalizes our results by estimating eq. (1) for 5 different bandwidths—50 km, 75 km, 100 km, 150 km and 200 km. The smallest of these bandwidths entails running the regression on 77 German counties closest to the former border, whereas the largest of these bandwidths runs the regression on 287 of the 401 counties in Germany.

Figure 2 – Discontinuity in log(1 + cases/million) at former border

Notes: Illustration of the discontinuity log(1 + cases/million people) across the former border between West and East Germany. The figure shows non-parametric local polynomial estimates for bins of the dependent variable, where each bin is 20 km wide. 95% confidence intervals are shaded in grey.

The latter three correspond to the range of the optimal bandwidths discussed in Section 3.[16] Different bandwidths alter the variance-bias trade-off in the RD point estimate. The degree of misspecification error is essentially controlled by the choice of bandwidth. Smaller than optimal, or undersmoothed, bandwidths create less bias in conventional confidence intervals than large bandwidths (Calonico et al., 2014), which is why we emphasize the results for 100 km or less. We see that the estimate for a 100 km bandwidth is a drop of -0.83 log points, or 57% of the cumulative COVID-19 case count as one crosses the border from West to East. This estimate is robust and statistically significant at 99% across bandwidths, ranging from -0.71 for a bandwidth of 75 km to -0.89 for a bandwidth of 200 km.[17]

The second row of Table 2 shows that there is also a discontinuity in COVID-19 deaths per million residents, which is larger in size than the discontinuity in the cumulative COVID-19 cases (although the estimates are noisier and the confidence intervals overlap because deaths are a small fraction of cases). For a 100 km bandwidth, crossing the border from west to east entails a 1.05 log point (65% decrease) in the number of deaths per million residents, with estimates for wider bandwidths showing a 50% larger drop.

[16] These bandwidths were computed for specifications without border segment fixed effects, whereas eq. (1) always includes border segment fixed effects.

[17] We present additional robustness of the discontinuity in cumulative COVID-19 cases to alternative functional forms of the local polynomial in Table B-1 of the Appendix.

Table 2 – Discontinuities in cases, deaths and other variables

	The dependent variable varies by panel				
	The bandwidth is				
	50 km	75 km	100 km	150 km	200 km
	(1)	(2)	(3)	(4)	(5)
Panel A. Log(1+cases/million)					
East	-.787***	-.710***	-.830***	-.987***	-.890***
	(.240)	(.149)	(.154)	(.196)	(.143)
Panel B. Log(1+deaths/million)					
East	-.963**	-.860***	-1.05***	-1.48***	-1.59***
	(.488)	(.308)	(.290)	(.423)	(.201)
Panel C. Disposable income p.c.					
East	-.084***	-.100***	-.104***	-.128***	-.134***
	(.026)	(.014)	(.005)	(.015)	(.014)
Panel D. Population density					
East	-.692**	-.584***	-.659***	-.474***	-.102
	(.279)	(.097)	(.230)	(.154)	(.193)
Panel E. Percent older than 64					
East	2.585***	2.175***	2.424***	3.132***	3.109***
	(.889)	(.830)	(.658)	(.616)	(.613)
Panel F. Percent older than 45 and younger than 65					
East	2.251***	1.653***	2.105***	1.714***	.992**
	(.778)	(.567)	(.546)	(.478)	(.445)
Panel G. Age-adjusted overall death rate per million					
East	.057***	.048**	.045**	.059***	.041*
	(.018)	(.020)	(.020)	(.016)	(.023)
Panel H. Age-adjusted infectious diseases death rate per million					
East	2.048**	1.723*	2.190**	2.630**	2.688**
	(.841)	(.998)	(1.087)	(1.146)	(1.119)
Panel I. Age-adjusted respiratory diseases death rate per million					
East	2.613**	2.191*	2.785**	3.216**	3.310**
	(1.109)	(1.258)	(1.372)	(1.457)	(1.437)
Observations	77	106	138	203	287

Notes: The table reports results from a regression discontinuity specification with an interacted local linear RD polynomial and border segment fixed effects. Disposable income per capita and population density are measured in logs. Standard errors clustered on the state (*Bundesländer*) level are reported in parentheses.

Discontinuities in control variables: It is well known that while West and East Germany have been reunified for 30 years, there are still considerable differences between the two territories. Alesina and Fuchs-Schündeln (2007) document persistent differences in trust, and Fuchs-Schündeln and Hassan (2015) show that many important economic variables are still discontinuous at the border.

In the remainder of Table 2 we investigate these additional discontinuities to assess whether they may explain the discontinuity in COVID-19 intensity that we have observed in the previous subsection. We see that regardless of the bandwidth used in the 50 km–200 km range, log population density, log disposable income, the share of the population aged 45 to 64 and the share older than 64, the date that the first COVID-19 case was recorded, and age-adjusted mortality from all causes, infectious diseases and respiratory diseases all show discontinuities at the old border. This fact alone complicates the interpretation of the discontinuity in cumulative COVID-19 cases as causal, and raises the possibility that it may be driven by some of these variables and not by an inherent characteristic of East Germans, such as BCG vaccination.

It is noteworthy that the signs of the discontinuities indicate that counties just to the east of the border have lower population density, lower consumption, an older population, a later introduction of COVID-19 and higher age-adjusted mortality rates than counties just to the west of the border. Intuitively, all of these factors, except for population density, should lead one to expect that counties just to the east should have a higher COVID-19 prevalence than counties just to the west. However, as we show in Table B-2 in the Appendix, both within the former East Germany and within the former West Germany, the raw correlations between cumulative COVID-19 cases and consumption per capita, population age and age-adjusted mortality rates all point in the "wrong" direction. For example, the correlation between log consumption per capita and log cumulative COVID-19 cases per capita is positive, while the correlations between log cumulative cases and age or mortality variables are generally negative. This suggests that the geography of the early outbreak in Germany was very particular. Indeed, some of the first cases in Bavaria were imported during the winter sports season from Italy and Austria, while early cases in the southwest can be linked to carnival celebrations. The virus then spread quickly through comparatively young and affluent counties—an issue to which we return below. While a similar pattern currently holds across US counties (where affluent and urban areas were exposed first), there are first signs that these correlations may ultimately reverse. The highest case counts per capita within New York City, for example, are in the poorer zip codes of Brooklyn, Queens and the Bronx, while upper-class zip codes have fewer cases.[18]

[18] See www.time.com/5815820/data-new-york-low-income-neighborhoods-coronavirus/.

Table 3 – Regression discontinuity results with controls

	The dependent variable is log(1+cases/million)				
	The bandwidth is				
	50 km	75 km	100 km	150 km	200 km
	(1)	(2)	(3)	(4)	(5)
Panel A. No Controls					
East	-.787***	-.710***	-.830***	-.987***	-.890***
	(.240)	(.149)	(.154)	(.196)	(.143)
Panel B. Population density					
East	-.750***	-.673***	-.807***	-.979***	-.887***
	(.220)	(.155)	(.183)	(.203)	(.144)
Panel C. Disposable income p.c.					
East	-.675***	-.605***	-.661***	-.814***	-.682***
	(.256)	(.189)	(.171)	(.200)	(.177)
Panel D. Disposable income p.c. and population density					
East	-.606**	-.537**	-.602**	-.782***	-.654***
	(.243)	(.232)	(.242)	(.238)	(.193)
Panel E. Percent older than 45 but younger than 65 and percent older than 64					
East	-.582***	-.530***	-.717***	-.804***	-.694***
	(.159)	(.104)	(.158)	(.175)	(.165)
Panel F. Controls from panels D and E					
East	-.411**	-.384**	-.442**	-.591***	-.498**
	(.181)	(.160)	(.183)	(.212)	(.199)
Panel G. Days since first case					
East	-.777***	-.698***	-.813***	-.972***	-.858***
	(.241)	(.153)	(.156)	(.198)	(.148)
Panel H. Age-adjusted overall death rate per million					
East	-.717***	-.646***	-.740***	-.875***	-.798***
	(.216)	(.143)	(.151)	(.205)	(.160)
Panel I. Age-adjusted infectious diseases death rate per million					
East	-.673**	-.607***	-.640***	-.786***	-.740***
	(.274)	(.142)	(.135)	(.157)	(.134)
Panel J. Age-adjusted respiratory diseases death rate per million					
East	-.648**	-.591***	-.614***	-.757***	-.708***
	(.268)	(.140)	(.125)	(.151)	(.128)
Observations	77	106	138	203	287

Notes: The table reports results from a regression discontinuity specification with an interacted local linear RD polynomial and border segment fixed effects. Disposable income per capita and population density are measured in logs. Standard errors clustered on the state (*Bundesländer*) level are reported in parentheses.

For each of the control variables analyzed in Table 2, we present evidence that the discontinuity in cumulative COVID-19 cases remains after adding the control variable in eq. (1). Table 3 presents the results. Panel A replicates the estimates without controls for reference. We see that irrespective of which additional variable is controlled for and regardless of the bandwidth used the estimate of the discontinuity in cumulative COVID-19 cases—the coefficient β in eq. (1)—remains negative and statistically significant at least at 5%. Only the magnitude declines somewhat across the different specifications. Even including multiple controls in the same regression—as in Panel F, where we include log disposable income per capita, log population density and percentages of the population above 45 and above 65—does not render the discontinuity in cumulative COVID-19 cases statistically insignificant. However, the magnitude of the RD coefficient falls by half, suggesting that these variables might play some role in explaining the East-West differential.

On balance, the evidence so far shows that there is a discontinuity in the intensity of COVID-19 across the former border separating East and West Germany, which is not primarily mediated by many of the channels one might have anticipated ex ante (or which were suggested by the German news media). We now turn to investigating potential explanations for this discontinuity, and specifically to the question of whether the discontinuity could be coming from greater BCG vaccination in former East Germany.

Age-specific regression discontinuity and RD-DD results: We now leverage the fact that different cohorts were vaccinated in the different parts of Germany to assess whether the BCG vaccine plays any role in this robust discontinuity for overall cases. The Robert Koch Institute provides age category breakdowns for county-level data on COVID-19 cases and deaths allowing us to obtain county-specific case and death totals for individuals aged 15–34 and individuals aged 35–59. As discussed earlier, if the discontinuity in COVID-19 cases is caused by the direct long-term effect of BCG vaccination, then we would expect that discontinuities in detected cases among people aged 15–34 should be close to zero (as most of them were never vaccinated in either part of Germany) while discontinuities among people aged 35–59 should be nonzero (since all of whom were vaccinated in the East but only those above 45 in the West). Given assessments in the medical community, we do not presume that spillovers to unvaccinated parts of the population would play a large role.[19]

Table 4 presents estimates of the discontinuity in cumulative COVID-19 cases per capita by age group. Panel A reproduces the baseline estimates. The next two rows present

[19]In the best case, having received the BCG vaccine bolsters the immune response to COVID-19 so that individuals display fewer symptoms (Curtis et al., 2020). Whether this implies that their viral load is lower so that they would infect fewer people, or whether the exact opposite would happen because they are more likely to be asymptomatic and feel "safe" is not clear at this point.

discontinuities for age groups 0–4 and 5–14. Individuals in both of these groups are unvaccinated on both sides of the former border, so that we should expect no discontinuity if BCG vaccination were to drive the difference. Instead, we observe statistically significant negative discontinuities in COVID-19 cases per capita for each of these groups. Moreover, these discontinuities are much larger in magnitude than the baseline discontinuity shown in Panel A. This evidence does not align with the BCG hypothesis. However, we are reluctant to place a lot of weight on them, since there are few COVID-19 cases in children younger than 15.

Panel D of Table 4 presents discontinuity estimates for individuals aged between 15 and 34. Roughly a quarter of COVID-19 cases in Germany involve people in this age group, so that the concern about drawing conclusions from too few data points does not apply. Once again, there are statistically significant negative discontinuities in cases per capita as one crosses the old border from west to east. Moreover, the magnitudes of these discontinuities are larger than the magnitudes of these discontinuities for the population as a whole (in Panel A). Panel E presents estimates for individuals between 35 and 59. Half of these individuals were vaccinated in West Germany while all of them were vaccinated in East Germany. Accordingly, we would expect this population to exhibit the largest discontinuity in COVID-19 cases per capita if the broad BCG hypothesis were true. However, while the discontinuities are large, statistically significant and negative, they are slightly smaller than the discontinuities for the whole population, let alone the 15–34 and 5–14 age groups. We present graphical illustrations of these discontinuities in Figure 3.

The results for the RD-DD specification which formalizes this comparison are presented in Panel H of Table 4. Recall that the coefficient of interest is γ. It captures the additional effect of being in the East on cumulative cases per million among the 35–59 population compared to the 15–34 cohort. This specification underlines that there is no statistically significant difference in COVID-19 prevalence across these two cohorts in spite of the abrupt change in BCG vaccination. Instead, the estimated effect is positive and equal to approximately a third of the baseline effect for the 15–34 population. Hence it appears that, if anything, the 35–59 year old population in the East is more vulnerable to infections with the novel coronavirus relative to their peers in the West. All of the available evidence points in the direction of a larger discontinuity in COVID-19 cases per capita for populations that were unvaccinated on both sides of the former border. Again, this fact is inconsistent with the empirical predictions of the BCG hypothesis.

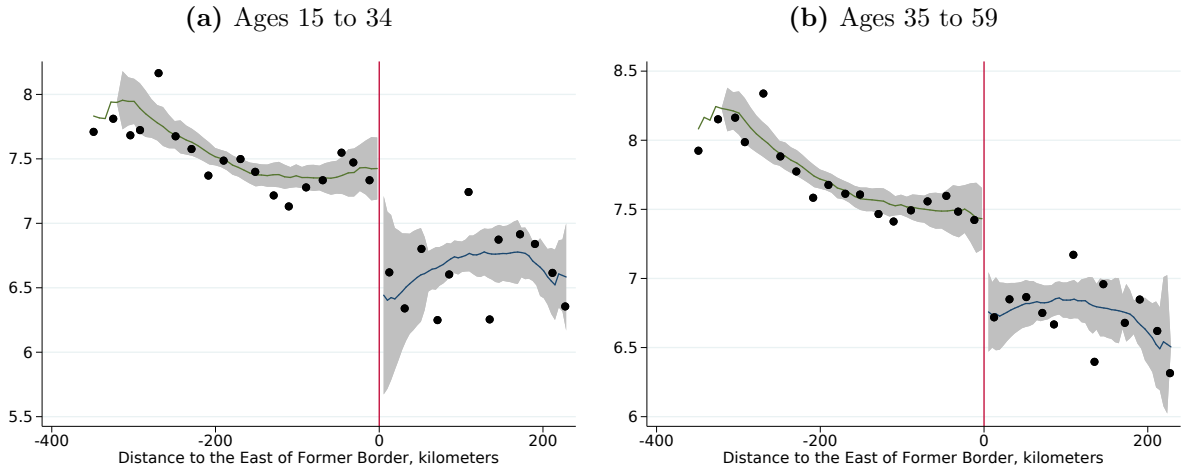
Placebo simulation with commuting patterns: If the BCG vaccine does not explain the East-West differential in coronavirus cases, then what does? A potential answer can

Table 4 – Regression discontinuity by age group and RD-DD

	The dependent variable varies by panel				
	The bandwidth is				
	50 km	75 km	100 km	150 km	200 km
	(1)	(2)	(3)	(4)	(5)
Panel A. All cases					
East	-.787***	-.710***	-.830***	-.987***	-.890***
	(.240)	(.149)	(.154)	(.196)	(.143)
Panel B. Cases for ages 00-04					
East	-1.59	-1.81**	-2.11***	-2.44***	-1.49***
	(1.049)	(.831)	(.606)	(.637)	(.511)
Panel C. Cases for ages 05-14					
East	-3.42***	-2.53***	-2.72***	-2.83***	-2.04**
	(.582)	(.605)	(.783)	(.776)	(.814)
Panel D. Cases for ages 15-34					
East	-1.04**	-.937*	-1.10*	-1.18**	-.993***
	(.464)	(.496)	(.570)	(.461)	(.278)
Panel E. Cases for ages 35-59					
East	-.685***	-.610***	-.732***	-.848***	-.770***
	(.166)	(.104)	(.128)	(.181)	(.151)
Panel F. Cases for ages 60-79					
East	-.678**	-.719***	-.858***	-1.07***	-1.06***
	(.302)	(.125)	(.093)	(.189)	(.113)
Panel G. Cases for ages 80p					
East	-.984**	-.928*	-1.33**	-1.72***	-1.63***
	(.434)	(.535)	(.533)	(.412)	(.276)
Panel H. RD-DD on age 15-34 and 35-59					
East × Old	.363	.327	.370	.337	.223
	(.391)	(.426)	(.486)	(.349)	(.246)
Observations	77	106	138	203	287

Notes: The table reports results from a regression discontinuity specification with an interacted local linear RD polynomial and border segment fixed effects. Standard errors clustered on the state (*Bundesländer*) level are reported in parentheses.

Figure 3 – Age-specific discontinuity in log(1 + cases/million at former border



Notes: Illustration of the discontinuity log(1 + cases/million people) across the former border between West and East Germany for different age groups. Panel a) shows results for ages 15 to 34 and panel b) shows results for ages 35 to 59. Both figures shows non-parametric local polynomial estimates for bins of the dependent variable, where each bin is 20 km wide. 95% confidence intervals are shaded in grey.

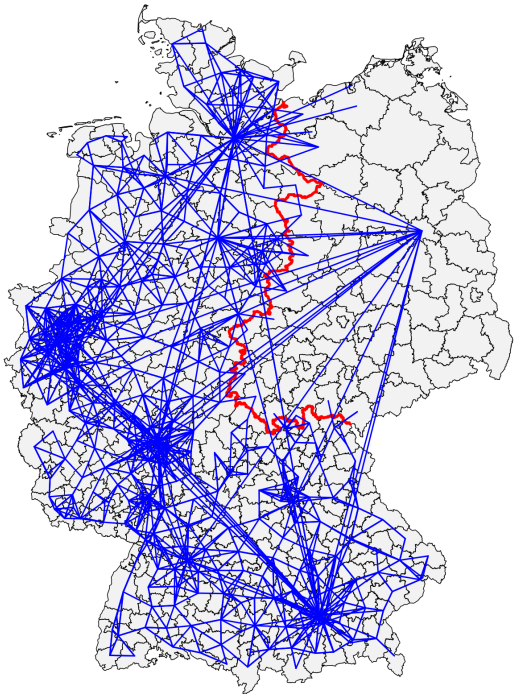
be found in Germany's regional connectedness. If those who live in the west work in the west and those who live in the east work in the east, it may be the case that travel flows have not readjusted completely since reunification. In other words, western counties along the former border may be disproportionately disconnected to their eastern neighbors than if there never would have been a national border dividing them. Although commuting over long distances is very common in Germany—almost 40% of jobs were in a different county than the primary residence—decades of partition meant that its infrastructure was re-oriented to connect counties within the west or east (Santamaria, 2020), with lasting effects on the spatial equilibrium in Germany.[20] As the epidemic started in the west, it may have had a harder time spreading eastward because relatively fewer people commute from west to east than commute across comparable distances within the west. The eastward spread was then further interrupted by the nation-wide lock-down on March 22 2020.

Figure 4a presents major outgoing commuter flows (more than 1,000 commuters per county) originating in what used to be West Germany. We see that our expectation is confirmed: almost all of them also go to the West. The only major destination in former East Germany is Berlin (neither Dresden nor Leipzig receive significant inflows from the west

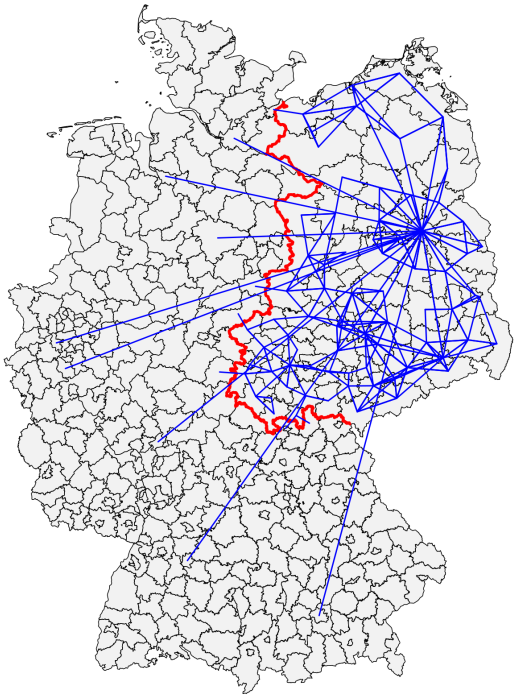
[20]Large infrastructure projects try to overcome this pattern since reunification but it is, for example, still difficult to reach Dresden from Cologne (or anywhere in the Ruhrgebiet) by public transport. Similarly, the Berlin–Munich high-speed rail connection was under construction since 1996 and only achieved modern speeds close to 4 hours in December 2017. Both distances are slightly less than 600 km.

Figure 4 – Major commuting flows (at least 1,000 people) by origin

(a) Originating in west



(b) Originating in east



Notes: Illustration of major commuter flows origination in the former FRG and former GDR based on the December 2019 commuting flows published by the Federal Employment Agency (*Bundesagentur für Arbeit*). For the purposes of this map, Berlin is geographically considered to be a part of the East.

but some counties on the eastern side of the old border receive some non-negligible flows). Similarly, in Figure 4b we see that major outgoing commuter flows originating in former East Germany also generally terminate in the East, again with the exception of significant flows from the capital to other western major cities. This holds in spite of a large wave of migration from East to West post-reunification. In fact, some of these flows are government workers who officially commute between Bonn, the old capital of the FRG which retained some government functions, and Berlin.

Table 5 puts these figures into our RD framework and presents discontinuity estimates for the fraction of incoming commuter flows that originate in West Germany at the county-level. Panel A shows that counties just to the east of the border receive between 32 and 72 percentage points more of their commuter flows from East Germany than do counties just to the west of the border. The standard errors are relatively small, so that these estimates are significant at all conventional levels. In Panel B of Table 5 we add this fraction of commuters from the West to our baseline regression for COVID-19 cases per capita across all age groups. This has a comparatively strong effect on the results. The RD coefficient at the reference

Table 5 – Regression discontinuity results with commuting and simulated results

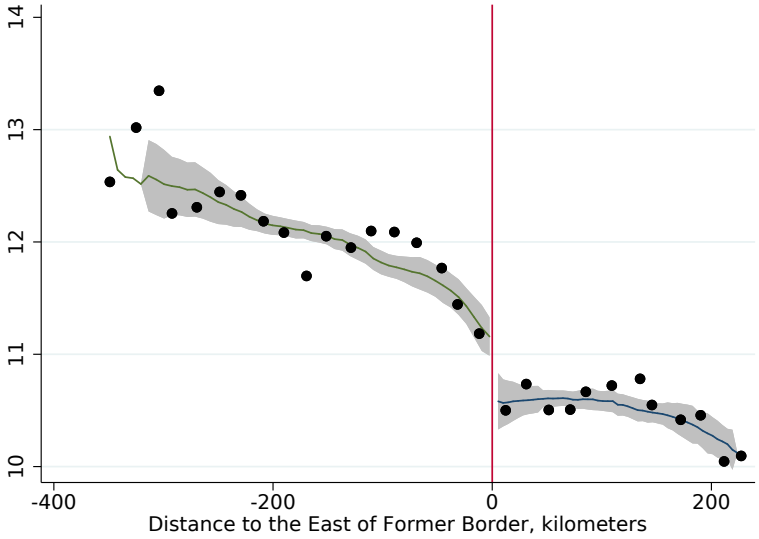
	The dependent variable is log(1+cases/million)				
	The bandwidth is				
	50 km	75 km	100 km	150 km	200 km
	(1)	(2)	(3)	(4)	(5)
Panel A. Fraction of incoming flows from West					
East	-.354***	-.475***	-.555***	-.669***	-.720***
	(.027)	(.026)	(.022)	(.020)	(.021)
Panel B. Log(1+cases/million), controlling for flows from West					
East	-.544***	-.363**	-.349*	-.322	-.350
	(.187)	(.166)	(.202)	(.200)	(.224)
Panel C. Log(1+cases/million), controlling for income, demographics and flows from West					
East	-.320	-.171	-.075	-.160	-.242
	(.220)	(.166)	(.231)	(.252)	(.248)
Panel D. Log(1+simulated cases/million)					
East	-.438*	-.493*	-.588**	-.866***	-.862***
	(.227)	(.254)	(.235)	(.245)	(.222)
Observations	77	106	138	203	287

Notes: The table reports results from a regression discontinuity specification with an interacted local linear RD polynomial and border segment fixed effects. Standard errors clustered on the state (*Bundesländer*) level are reported in parentheses.

bandwidth of 100 km falls by almost 0.5 log points and is only marginally significant at 10%. At higher bandwidths, the effect is no longer significant at conventional levels. This is a larger impact than controlling for log disposable income per capita, log population density and the age distribution at the same time. In Panel C we also add log population density, the age distribution as well as log disposable income (the controls from Panel E of Table 3). Now the effect becomes numerically small at the reference bandwidth and insignificant for the entire range of bandwidths. In other words, accounting for only differences in mobility and demographics is enough for the discontinuity in cases to disappear.

Our final exercise demonstrates that mobility patterns, population differences and the geography of the initial outbreaks can create a counterfactual discontinuity just like the one we observe in the actual data. We simulate a canonical SIR model of the coronavirus epidemic in each German county with mobility flows following Wesolowski et al. (2017) and Bjørnstad and Grenfell (2008). In the model, we allow infections to spread along commuting patterns starting from the distribution of coronavirus cases on February 29 2020 and use the approximate epidemiological characteristics of the outbreak in Germany (e.g., a reproduction number, R_0 of 2.5). We use the observed commuting flows from December 2019 together with

Figure 5 – Discontinuity in log(1 + simulated cases/million) at former border



Notes: Illustration of the discontinuity log(1 + simulated cases/million people) across the former border between West and East Germany. The simulation and its underlying parameters are described in Appendix A. The figure shows non-parametric local polynomial estimates for bins of the dependent variable, where each bin is 20 km wide. 95% confidence intervals are shaded in grey.

county population data to proxy for actual mobility around the time of the outbreak. We simulate the model for 60 periods (days) but stop all commuting flows after 22 days to reflect the nation-wide shutdown. The details of the simulation are provided in Appendix A.[21]

Panel D of Table 5 presents the discontinuity estimates for the simulated log cumulative cases per capita. We find that in the simulated data, the number of cases also discontinuously declines as one crosses from west to east over the former border. The decline is somewhat smaller, but close in magnitude, to the decline observed in the actual data. This confirms the results of the RD design with controls for commuter flows and strongly suggests that mobility is a key driver of the geography of the early outbreak. Our methodology cannot exclude other alternative explanations, and officially registered commuter flows likely do not represent person-to-person movement across Germany perfectly. However, our simulation constructs a situation that shares some essential features of the data, and that explains the discontinuously lower novel coronavirus prevalence across the border into the former East without reference to the (broad) BCG hypothesis. This fact together with the pattern in the discontinuities across cohorts, leaves us very skeptical that the BCG vaccine plays a role in explaining the geography of the outbreak in Germany.

[21] The simulation overpredicts the overall case count because we do not explicitly model social distancing (apart from the lack of commuting). In the observed data, the reproduction number declined toward unity over the same period.

5 Conclusion

Our paper provides a cautionary tale of potentially misleading correlations, which appear early in the outbreak of an epidemic. Using the modern applied econometrics toolkit, we show that there is a stark break in cumulative COVID-19 cases at the former border which used to separate East and West Germany. However, our analysis strongly suggests that an appealing explanation—the variation in BCG vaccination status for large populations across the border—cannot account for this discontinuity. Instead, more mundane factors appear to be behind this East-West differences. Accounting for commuter flows, income and demographics is sufficient for the difference to vanish. These results help to address the identification problems encountered in the scientific and journalistic debate on the merits of the BCG hypothesis.

Our findings have several important limitations. First, they are derived from the context of Germany, the health profile of its population, and the specific strains of COVID-19 circulating there, and therefore may not be as applicable to other parts of the world. Second, they cannot speak to the possibility of a short-run boost to the immune system coming from the BCG vaccine that may offer individuals some "trained immunity" against COVID-19. In particular, our results should not be taken to anticipate the outcomes of the clinical trials that are currently taking place. Third, our study looks at a summary measure of the intensity of the epidemic—cumulative case counts per capita—and does not consider in detail other dimensions, such as the lethality of infections or the speed of transmission from the infected to the susceptible.

While it is disappointing to find evidence against a partial remedy, we believe that negative results are necessary for the world to redeploy resources in the right direction. They also help guard against a false sense of security that countries with a current BCG vaccination policy might feel. To the extent that current case counts around the globe are a product of the early geography of the pandemic rather than of immutable features of populations, less affected countries and regions should take their reprieve as a time to prepare rather than as a time for complacency. It is not unimaginable that the raw discontinuity we documented will eventually disappear or even turn around if the infection spreads to a poorer, older and more disease-prone population in the East.

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A SIR Model with commuter flows

We simulate a SIR model with multiple locations and exogenous migration flows between locations. This model has been used in Wesolowski et al. (2017) and Bjørnstad and Grenfell (2008). It is described by four difference equations

$$\tilde{I}_{j,t} = I_{i,t} + \frac{N_i \sum_j m_{j,i} \frac{I_{j,t}}{N_j}}{N_i + \sum_j m_{j,i}} \tag{A-1}$$

$$S_{i,t+1} = S_{i,t} - \beta S_{i,t} \frac{\tilde{I}_{i,t}}{N_i} \tag{A-2}$$

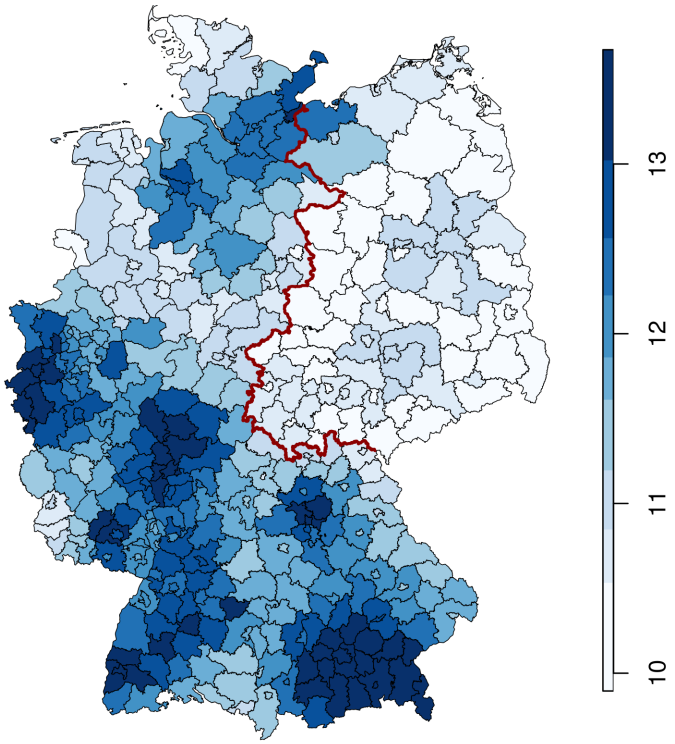
$$I_{i,t+1} = I_{i,t} + \beta S_{i,t} \frac{\tilde{I}_{i,t}}{N_i} - \gamma I_{i,t} \tag{A-3}$$

$$R_{i,t+1} = R_{i,t} + \gamma I_{i,t} \tag{A-4}$$

where $m_{j,i}$ is the number of commuters going from location j to location i each period and all other variables are as in the classical SIR model. We take German counties as the locations in our models. We assume $\gamma = 1/7$ (because the incubation period is 7 days on average, and much of the transmission is pre-symptomatic) and $R_0 = \beta/\gamma = 2.5$. We assume the initial counts of infected to correspond to the reported cases by county on February 29. We simulate the model for 60 time periods, assuming that after time period 22, all cross-county commuting flows are shut down to simulate measures taken by the German government.

We have tried other parametrizations of the SIR model and we get similar results provided that the epidemic is not allowed to evolve too close to the long-run equilibrium (which, when migration flows are eventually shut down, is the same for each county and hence, would not generate a discontinuity). The magnitude of the case counts resulting from the epidemic vary widely between parametrizations. We view this exercise not as an attempt to model the COVID-19 epidemic in Germany but to provide an illustration that mobility patterns can generate discontinuities in the spread of an epidemic without there being essential discontinuities in the underlying epidemic resistance of the population.

Figure A-1 – Counterfactual COVID-19 cases in Germany, end of April



Notes: Illustration of the simulated spatial distribution of an epidemic with the parameters described in the Appendix, the same starting distribution across German counties as cumulative COVID-19 cases on Feb. 29, 2020; and following the December 2019 commuting flows published by the Federal Employment Agency (*Bundesagentur für Arbeit*). The map shows the log(1 + simulated cases/million people) in each county using population data from 2018.

B Appendix Tables

Table B-1 – Regression discontinuity estimates for various approximating polynomials

	The dependent variable is log(1+cases/million)				
	The bandwidth is				
	50 km	75 km	100 km	150 km	200 km
	(1)	(2)	(3)	(4)	(5)
Panel A. Interacted linear polynomial in distance to the border					
East	-.787***	-.710***	-.830***	-.987***	-.890***
	(.240)	(.149)	(.154)	(.196)	(.143)
Panel B. Linear polynomial in distance to the border					
East	-.670*	-.718***	-.889***	-.985***	-.898***
	(.357)	(.119)	(.128)	(.145)	(.168)
Panel C. Linear polynomial in latitude and longitude					
East	-.805***	-.911***	-1.03***	-1.00***	-.928***
	(.112)	(.092)	(.102)	(.088)	(.077)
Panel D. Interacted cubic polynomial in distance to the border					
East	-.432	-1.09**	-1.44***	-.708**	-.776***
	(.540)	(.528)	(.216)	(.306)	(.231)
Panel D. Cubic polynomial in distance to the border					
East	-1.15***	-.767**	-.614**	-.880***	-.975***
	(.395)	(.378)	(.259)	(.141)	(.133)
Panel E. Cubic polynomial in latitude and longitude					
East	-.768***	-.822***	-.999***	-1.21***	-1.20***
	(.206)	(.100)	(.091)	(.131)	(.113)
Observations	77	106	138	203	287

Notes: The table reports results from a regression discontinuity specification with an interacted local linear RD polynomial and border segment fixed effects. Standard errors clustered on the state (*Bundesländer*) level are reported in parentheses.

Table B-2 – OLS Correlations between COVID-19 Cases and Control Variables

	The dependent variable is log(1+cases/million)		
	The sample is		
	West	East	All
	(1)	(2)	(3)
Disposable income p.c.	2.38***	3.43*	3.38***
	(.74)	(1.99)	(.60)
Population density	-.03	.15***	.08
	(.08)	(.02)	(.07)
Percent older than 64	-.08***	-.01	-.12***
	(.03)	(.06)	(.02)
Percent older than 45 and younger than 65	-.01	-.04***	-.06***
	(.01)	(.00)	(.02)
Age-adjusted overall death rate	-2.56**	-2.96***	-3.38***
	(1.10)	(.87)	(.87)
Age-adjusted infectious diseases death rate	-20.33**	-2.55	-23.04*
	(8.88)	(14.19)	(13.34)
Age-adjusted respiratory death rate	-8.79***	-3.14	-9.88***
	(1.77)	(5.17)	(1.90)
Observations	324	76	400

Notes: The table reports results from ordinary least squares regressions for the samples indicated in the column headers. Standard errors clustered on the state (*Bundesländer*) level are reported in parentheses.